



SEQUENCE LISTING

<110> Gravel, Roy A,
Rozen, Rima
Leclerc, Daniel
Wilson, Aaron
Rosenblatt, David

<120> HUMAN METHIONINE SYNTHASE REDUCTASE:
CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
DEFECTS, CARDIOVASCULAR DISEASE, CANCER, AND DOWN'S SYNDROME

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 <213> *Vigna radiata*

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<210> 30
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 <213> *Aspergillus niger*

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<210> 31
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 <213> *Homo sapiens*

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 <213> *Thiocapsa roseopersicina*

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<210> 39
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<213> Homo sapiens

<400> 41

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<211> 698

<212> PRT

<213> Homo sapiens

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Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
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 <212> DNA
 <213> Homo sapiens

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Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly	450	455	460
Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr	465	470	475
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Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn	515	520	525
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Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu	545	550	555
Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu	565	570	575
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gcaaagtatg tacaagacaa catccagctt catggccagc aggtggcgag aatcctcctc 1920
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gatgcccttg tgcaaataat aagcaaagag gttggagttg aaaaactaga agcaatgaaa 2040
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<210> 46

<211> 697

<212> PRT

<213> Homo sapiens

<400> 46

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Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
          35          40          45
Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
          50          55          60
Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
65          70          75          80
Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
          85          90          95
Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
          100         105         110
Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
          115         120         125
Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
          130         135         140
Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
          145         150         155         160
Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg

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Thr	Asp	Leu	Val	165	Lys	Ser	Glu	Leu	Leu	170	His	Ile	Glu	Ser	Gln	175	Val	Glu
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Leu	Leu	Arg	Phe	Asp	Asp	Ser	Gly	Arg	Lys	Asp	Ser	Glu	Val	Leu	Lys			
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Gln	Asn	Ala	Val	Asn	Ser	Asn	Gln	Ser	Asn	Val	Val	Ile	Glu	Asp	Phe			
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Glu	Ser	Ser	Leu	Thr	Arg	Ser	Val	Pro	Pro	Leu	Ser	Gln	Ala	Ser	Leu			
225					230						235				240			
Asn	Ile	Pro	Gly	Leu	Pro	Pro	Glu	Tyr	Leu	Gln	Val	His	Leu	Gln	Glu			
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Ser	Leu	Gly	Gln	Glu	Glu	Ser	Gln	Val	Ser	Val	Thr	Ser	Ala	Asp	Pro			
		260					265						270					
Val	Phe	Gln	Val	Pro	Ile	Ser	Lys	Ala	Val	Gln	Leu	Thr	Thr	Asn	Asp			
	275						280						285					
Ala	Ile	Lys	Thr	Thr	Leu	Leu	Val	Glu	Leu	Asp	Ile	Ser	Asn	Thr	Asp			
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Phe	Ser	Tyr	Gln	Pro	Gly	Asp	Ala	Phe	Ser	Val	Ile	Cys	Pro	Asn	Ser			
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Asp	Ser	Glu	Val	Gln	Ser	Leu	Leu	Gln	Arg	Leu	Gln	Leu	Glu	Asp	Lys			
			325					330						335				
Arg	Glu	His	Cys	Val	Leu	Leu	Lys	Ile	Lys	Ala	Asp	Thr	Lys	Lys	Lys			
		340					345						350					
Gly	Ala	Thr	Leu	Pro	Gln	His	Ile	Pro	Ala	Gly	Cys	Ser	Leu	Gln	Phe			
	355					360						365						
Ile	Phe	Thr	Trp	Cys	Leu	Glu	Ile	Arg	Ala	Ile	Pro	Lys	Lys	Ala	Phe			
	370				375						380							
Leu	Arg	Ala	Leu	Val	Asp	Tyr	Thr	Ser	Asp	Ser	Ala	Glu	Lys	Arg	Arg			
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Leu	Gln	Glu	Leu	Cys	Ser	Lys	Gln	Gly	Ala	Ala	Asp	Tyr	Ser	Arg	Phe			
			405					410						415				
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		420					425						430					
Ser	Cys	Gln	Pro	Pro	Leu	Ser	Leu	Leu	Leu	Glu	His	Leu	Pro	Lys	Leu			
	435					440						445						
Gln	Pro	Arg	Pro	Tyr	Ser	Cys	Ala	Ser	Ser	Ser	Leu	Phe	His	Pro	Gly			
	450					455					460							
Lys	Leu	His	Phe	Val	Phe	Asn	Ile	Val	Glu	Phe	Leu	Ser	Thr	Ala	Thr			
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Thr	Glu	Val	Leu	Arg	Lys	Gly	Val	Cys	Thr	Gly	Trp	Leu	Ala	Leu	Leu			
			485					490						495				
Val	Ala	Ser	Val	Leu	Gln	Pro	Asn	Ile	His	Ala	Ser	His	Glu	Asp	Ser			
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Gly	Lys	Ala	Leu	Ala	Pro	Lys	Ile	Ser	Ile	Ser	Pro	Arg	Thr	Thr	Asn			
	515					520					525							
Ser	Phe	His	Leu	Pro	Asp	Asp	Pro	Ser	Ile	Pro	Ile	Ile	Met	Val	Gly			
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Pro	Gly	Thr	Gly	Ile	Ala	Pro	Phe	Ile	Gly	Phe	Leu	Gln	His	Arg	Glu			
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			565					570						575				
Phe	Gly	Cys	Arg	His	Lys	Asp	Arg	Asp	Tyr	Leu	Phe	Arg	Lys	Glu	Leu			
		580					585						590					
Arg	His	Phe	Leu	Lys	His	Gly	Ile	Leu	Thr	His	Leu	Lys	Val	Ser	Phe			
	595					600						605						
Ser	Arg	Asp	Ala	Pro	Val	Gly	Glu	Glu	Glu	Ala	Pro	Ala	Lys	Tyr	Val			
	610					615					620							

Gln	Asp	Asn	Ile	Gln	Leu	His	Gly	Gln	Gln	Val	Ala	Arg	Ile	Leu	Leu
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Gln	Glu	Asn	Gly	His	Ile	Tyr	Val	Cys	Gly	Asp	Ala	Lys	Asn	Met	Ala
				645						650					655
Lys	Asp	Val	His	Asp	Ala	Leu	Val	Gln	Ile	Ile	Ser	Lys	Glu	Val	Gly
			660						665					670	
Val	Glu	Lys	Leu	Glu	Ala	Met	Lys	Thr	Leu	Ala	Thr	Leu	Lys	Glu	Glu
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<210> 47
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 <212> DNA
 <213> Homo sapiens

<400> 47
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 ggcaccggag acccaccgga cacagcccgc aagtttggtta aggaaatata gaaccaaaca 240
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 agaaaggatt ctgaggtttt gaagcaaat gcagtgaaca gcaaccaatc caatgttgta 660
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 atgcccttgt gcaataata agcaaagggt ttggagttga aaaactagaa gcaatgaaaa 2040
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<210> 48
 <211> 689
 <212> PRT

<213> Homo sapiens

<400> 48

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		20					25						30		
Asp	Leu	His	Cys	Ile	Ser	Glu	Ser	Asp	Lys	Tyr	Asp	Leu	Lys	Thr	Glu
		35				40						45			
Thr	Ala	Pro	Leu	Val	Val	Val	Val	Ser	Thr	Thr	Gly	Thr	Gly	Asp	Pro
	50					55					60				
Pro	Asp	Thr	Ala	Arg	Lys	Phe	Val	Lys	Glu	Ile	Gln	Asn	Gln	Thr	Leu
65					70				75						80
Pro	Val	Asp	Phe	Phe	Ala	His	Leu	Arg	Tyr	Gly	Leu	Leu	Gly	Leu	Gly
			85						90					95	
Asp	Ser	Glu	Tyr	Thr	Tyr	Phe	Cys	Asn	Gly	Gly	Lys	Ile	Ile	Asp	Lys
		100						105					110		
Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	His	Phe	Tyr	Asp	Thr	Gly	His	Ala
		115					120						125		
Asp	Asp	Cys	Val	Gly	Leu	Glu	Leu	Val	Val	Glu	Pro	Trp	Ile	Ala	Gly
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Leu	Trp	Pro	Ala	Leu	Arg	Lys	His	Phe	Arg	Ser	Ser	Arg	Gly	Gln	Glu
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Glu	Ile	Ser	Gly	Ala	Leu	Pro	Val	Ala	Ser	Pro	Ala	Ser	Leu	Arg	Thr
			165						170					175	
Asp	Leu	Val	Lys	Ser	Glu	Leu	Leu	His	Ile	Glu	Ser	Gln	Val	Glu	Leu
		180						185					190		
Leu	Arg	Phe	Asp	Asp	Ser	Gly	Arg	Lys	Asp	Ser	Glu	Val	Leu	Lys	Gln
	195					200						205			
Asn	Ala	Val	Asn	Ser	Asn	Gln	Ser	Asn	Val	Val	Ile	Glu	Asp	Phe	Glu
	210					215					220				
Ser	Ser	Leu	Thr	Arg	Ser	Val	Pro	Pro	Leu	Ser	Gln	Ala	Ser	Leu	Asn
225					230					235					240
Ile	Pro	Gly	Leu	Pro	Pro	Glu	Tyr	Leu	Gln	Val	His	Leu	Gln	Glu	Ser
			245						250					255	
Leu	Gly	Gln	Glu	Glu	Ser	Gln	Val	Ser	Val	Thr	Ser	Ala	Asp	Pro	Val
		260						265					270		
Phe	Gln	Val	Pro	Ile	Ser	Lys	Ala	Val	Gln	Leu	Thr	Thr	Asn	Asp	Ala
		275					280						285		
Ile	Lys	Thr	Thr	Leu	Leu	Val	Glu	Leu	Asp	Ile	Ser	Asn	Thr	Asp	Phe
	290					295					300				
Ser	Tyr	Gln	Pro	Gly	Asp	Ala	Phe	Ser	Val	Ile	Cys	Pro	Asn	Ser	Asp
305					310					315					320
Ser	Glu	Val	Gln	Ser	Leu	Leu	Gln	Arg	Leu	Gln	Leu	Glu	Asp	Lys	Arg
			325						330					335	
Glu	His	Cys	Val	Leu	Leu	Lys	Ile	Lys	Ala	Asp	Thr	Lys	Lys	Lys	Gly
		340						345					350		
Ala	Thr	Leu	Pro	Gln	His	Ile	Pro	Ala	Gly	Cys	Ser	Leu	Gln	Phe	Ile
		355					360					365			
Phe	Thr	Trp	Cys	Leu	Glu	Ile	Arg	Ala	Ile	Pro	Lys	Lys	Ala	Phe	Leu
	370					375					380				
Arg	Ala	Leu	Val	Asp	Tyr	Thr	Ser	Asp	Ser	Ala	Glu	Lys	Arg	Arg	Leu
385					390					395					400
Gln	Glu	Leu	Cys	Ser	Lys	Gln	Gly	Ala	Ala	Asp	Tyr	Ser	Arg	Phe	Val
			405						410					415	
Arg	Asp	Ala	Cys	Ala	Cys	Leu	Leu	Asp	Leu	Leu	Leu	Ala	Phe	Pro	Ser
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Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu Gln
 435 440 445
 Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly Lys
 450 455 460
 Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr Thr
 465 470 475 480
 Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu Val
 485 490 495
 Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser Gly
 500 505 510
 Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn Ser
 515 520 525
 Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly Pro
 530 535 540
 Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Asn Ser
 545 550 555 560
 Lys Asn Asn Thr Gln Met Glu Ile Leu Glu Gln Cys Gly Cys Phe Leu
 565 570 575
 Ala Ala Gly Ile Arg Ile Gly Ile Ile Tyr Ser Glu Lys Ser Ser Asp
 580 585 590
 Ile Ser Leu Ser Met Gly Ser Leu Ile Arg Phe Pro Ser Gln Glu Met
 595 600 605
 Leu Leu Leu Gly Arg Arg Lys Pro Gln Gln Ser Met Tyr Lys Thr Thr
 610 615 620
 Ser Ser Phe Met Ala Ser Arg Trp Arg Glu Ser Ser Ser Arg Arg Thr
 625 630 635 640
 Ala Ile Phe Met Cys Val Glu Met Gln Arg Ile Trp Pro Arg Met Tyr
 645 650 655
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 Lys Pro Trp Pro Leu Lys Lys Lys Asn Ala Thr Phe Arg Ile Phe Gly
 675 680 685
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<210> 49
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 49
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23

<210> 50
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 50
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26

<210> 51
 <211> 2187
 <212> DNA
 <213> Homo sapiens

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<400> 51
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gagcggcatg agagactccg ggagaagatg aggcggcgat tggaaatctgg tgacaagtgg 180
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<210> 52
<211> 20
<212> PRT
<213> Homo sapiens

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20

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<210> 53
<211> 23
<212> PRT
<213> Homo sapiens

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<400> 53

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 Arg Lys Phe Val Lys Glu Ile
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<210> 54
 <211> 29
 <212> PRT
 <213> Homo sapiens

<400> 54
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<210> 55
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 <213> Homo sapiens

<400> 55
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<210> 56
 <211> 14
 <212> PRT
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<400> 56
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<210> 57
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 <212> PRT
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<400> 57
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<210> 58
 <211> 22
 <212> PRT
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<400> 58
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<210> 59
 <211> 6
 <212> PRT
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<400> 59
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<210> 60
 <211> 41
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<400> 60
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<210> 61
 <211> 26
 <212> DNA
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<400> 61
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<210> 62
 <211> 27
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<400> 62
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<210> 63
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 63
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